Ecology of Rickettsia in South America

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Until the year 2000, only three *Rickettsia* species were known in South America: (i) *Rickettsia rickettsii,* transmitted by the ticks *Amblyomma cajennense,* and *Amblyomma aureolatum*, reported in Colombia, Argentina, and Brazil, where it is the etiological agent of Rocky Mountain spotted fever; (ii) *Rickettsia prowazekii,* transmitted by body lice and causing epidemic typhus in highland areas, mainly in Peru; (iii) *Rickettsia typhi,* transmitted by fleas and causing endemic typhus in many countries. During this new century, at least seven other rickettsiae were reported in South America: *Rickettsia felis* infecting fleas and the tick-associated agents *Rickettsia parkeri, Rickettsia massiliae, Candidatus* "Rickettsia amblyommii," *Rickettsia bellii, Rickettsia rhipicephali,* and *Candidatus* "Rickettsia andeanae." Among these other rickettsiae, only *R. felis, R. parkeri,* and *R. massiliae* are currently recognized as human pathogens. *R. rickettsii* is a rare agent in nature, infecting ≤1% individuals in a few tick populations. Contrastingly, *R. parkeri, Candidatus* "R. amblyommii," *R. rhipicephali,* and *R. bellii* are usually found infecting 10 to 100% individuals in different tick populations. Despite rickettsiae being transmitted transovarially through tick generations, low infection rates for *R. rickettsii* are possibly related to pathogenic effect of *R. rickettsii* for ticks, as shown for *A. aureolatum* under laboratory conditions. This scenario implies that *R. rickettsii* needs amplifier vertebrate hosts for its perpetuation in nature, in order to create new lines of infected ticks (horizontal transmission). In Brazil, capybaras and opossums are the most probable amplifier hosts for *R. rickettsii,* among *A. cajennense* ticks, and small rodents for *A. aureolatum*.

***Key words*: *Rickettsia*; ecology; tick; lice; flea; South America**

Introduction

Until the year 2000, only three *Rickettsia* species were known to occur in South America, being two typhus group (TG) species (*Rickettsia prowazekii* and *Rickettsia typhi*) and only one spotted fever group (SFG) species (*Rickettsia rickettsii*). These three species are pathogenic for humans to whom *R. prowazekii* is transmitted by lice, *R. typhi* by fleas, and *R. rickettsii* by ticks. During this new century, at least 7 other *Rickettsia* species were reported in South America: *Rickettsia felis* infecting fleas in Argentina, Brazil, Chile, Peru, and Uruguay, *Rickettsia parkeri* infecting ticks in Uruguay and Brazil, *Rickettsia massiliae* infecting ticks in Argentina, *Candidatus* "Rickettsia amblyommii" infecting ticks in Argentina, Brazil, and French Guyana, *Rickettsia bellii* infecting ticks in Argentina and Brazil, *Rickettsia rhipicephali* infecting ticks in Brazil, and *Candidatus* "Rickettsia andeanae" infecting ticks in Peru. Among these, all species are classified into the SFG except for *R. bellii,* which in neither a TG nor a SFG species.

Rickettsia rickettsii

Rickettsia rickettsii is the most pathogenic *Rickettsia* species of the world.[1] It has been reported in Canada, United States, Mexico, Costa Rica, Panama, Colombia, Brazil, and Argentina.[2,3] The disease caused by *R. rickettsii* is generally

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called Rocky Mountain spotted fever (RMSF), because it was first reported in the Rocky Mountain region of the United States, but it is also called as Brazilian spotted fever (BSF) in Brazil. Different tick species have been implicated as vectors of *R. rickettsii* accordingly to different geographic areas. Whereas the ticks *Dermacentor andersoni* and *Dermacentor variablilis* are the main vectors in the United States,[2] *Amblyomma cajennense* has been implicated to be the most important vector in South America. *Amblyomma aureolatum* is also a recognized vector within the metropolitan area of São Paulo city,[4] where *Rhipicephalus sanguineus* is a suspected vector.[5]

RMSF has been reported in Brazil since the 1920s. After various reports during the 1930s and 1940s, much fewer reports were released from the 1950s to early 1980s. From the end of the 1980s to the beginning of the present century, there has been a clear re-emergence of the disease in Brazil. For example, from 1988 to 1997, there were 25 laboratory-confirmed cases distributed among 6 municipalities in the state of São Paulo. During the subsequent decade, from 1998 to 2007, there were 255 confirmed cases distributed among 54 municipalities of the state. Indeed, this increase is partially attributed to a much more efficient surveillance, especially after the disease became nationally notifiable in 2001. However, ecological factors seem to have played a major role, as discussed below. In the southeastern region of Brazil, composed by four states (São Paulo, Minas Gerais, Rio de Janeiro, and Espírito Santo), there were 334 laboratory-confirmed cases of RMSF from 1995 to 2004, with a 31% fatality-ratio. Only in the state of São Paulo, 128 additional cases (case fatality: 29%) were confirmed from 2005 to 2007 (official data from the São Paulo State Health Secretary).

A. cajennense is one of the most common tick species in southeastern Brazil, where it is far the most frequent human-biting tick. Comparing to *A. cajennense,* other tick species are seldom found biting humans in southeastern Brazil.[6] The most abundant primary hosts for *A. cajennense* in southeastern Brazil are horses and capybaras (*Hydrochoerus hydrochaeris*), which are infested by all tick's parasitic stages. Humans are also attacked by all parasitic stages, usually by hundreds of larvae, dozens of nymphs, or/and a few adult specimens. Fortunately, serologic-based studies on horses and capybaras (sentinels for RMSF within the distribution area of *A. cajennense* in Brazil) have indicated that very few populations of *A. cajennense* are infected by SFG rickettsiae.[7,8] This finding is corroborated by the low number of RMSF cases in the southeastern region of Brazil, in contrast to the large human population that is exposed to infestations by *A. cajennense* in almost the entire rural area of this region. Even in RMSF-endemic areas in Brazil, infection rates by *R. rickettsii* among *A. cajennense* populations are usually very low, around 1%,[9] or low enough for some studies to have failed to find a *R. rickettsii*-infected tick specimen.[7]

A. aureolatum has been implicated as the vector of *R. rickettsii* in the São Paulo metropolitan area since the 1930s.[10] The adult stage of this tick uses Carnivore species (mostly the domestic dog) as primary host while immature stages seem to use Passeriformes birds and a few rodent species as primary hosts.[11] Humans are attacked only by the adult stage, usually by a single adult tick, because population density of this tick species is usually low.[12] One recent study found 0.9% (6/669) *A. aureolatum* ticks to be infected by *R. rickettsii*.[4] In most of the sites of transmission of *R. rickettsii* by *A. aureolatum, A. cajennense* is scarce or absent, whereas *R. sanguineus* is sometimes abundant.[5,12]

In vertebrate hosts, *R. rickettsii* causes acute infection lasting for only a few days or weeks, with no persistent maintenance of the agent.[13] Thus, vertebrate hosts cannot be considered reservoirs of *R. rickettsii* in nature. Studies in the United States demonstrated that *R. rickettsii* is transmitted transovarially and transstadially in several tick species occurring in North America, including its main tick vectors *D. andersoni*, *D. variabilis*, and *R. sanguineus*.[2,13,14] These laboratory studies indicated that ticks

are the main reservoir of *R. rickettsii* in nature.[15] However, other factors must account for the usually low *R. rickettsii*-infection rates in ticks, ranging from 0.05 to 1.3% in the United States and Brazil.[4,7,9,13]

Burgdorfer and Brinton[16] and Nielbisky[17] showed that *R. rickettsii* displays some degree of pathogenicity to both *D. anndersoni* and *D. variabilis* ticks, thus uninfected ticks would have advantage over infected ticks in a tick population during consecutive generations. This rickettsial pathogenicity is possibly the major cause of very low infection rates of *R. rickettsii*-infected ticks in nature. Thus, even that ticks are the main reservoir of *R. rickettsii* in nature, the *R. rickettsii* pathogenicity for ticks precludes its enzootic maintenance solely by transovarial and transstadial transmissions in ticks.[17] In this case, the participation of amplifier hosts (vertebrate animals that develop a rickettsemia for some days) is crucial when new uninfected ticks become infected and start new lineages of infected ticks within the tick population.[2] In the United States, several small rodent species have been implicated to act as amplifier hosts of *R. rickettsii*, as for example, *Microtus pennsylvanicus* for *D. variabilis* in the eastern part of the country.[13,15,18]

In general, a vertebrate host species has to fulfill the following five requirements in order to be considered an efficient amplifier host for *R. rickettsii* in a given RMSF-endemic area:

1. It has to be abundant in the *R. rickettsii*-endemic area.
2. It has to be a major host for the tick vector.
3. It has to be susceptible to the *R. rickettsii* infection.
4. Once infected by *R. rickettsii,* the host has to develop a rickettsemia of sufficient length and degree to infect ticks that feed on this host.
5. It has to be a prolific species, in order to have a continuous introduction of nonimmune animals in the host population.

M. pennsylvanicus is an efficient amplifier host species for *R. rickettsii* in the United States because it is abundant in many *R. rickettsii*-endemic areas in the eastern part of the country, where it is also a primary host for the immature stages of *D. variablilis.*[15] In addition, *M. pennsylvanicus* has been shown to be highly susceptible to *R. rickettsii,* as it developed rickettsemia for 6 to 8 days in concentrations sufficient to infect nearly 100% of uninfected *Dermacentor* larvae that fed on them.[18] Finally, as any other small rodent, *M. pennsylvanicus* is highly prolific, as average females have between one and five litters in a year, producing about five pups in each litter.[19] This last requirement is very important if one considers that once living in an endemic area, each individual host will develop only one rickettsemia (lasting for a few days or weeks) during its lifetime, since after the rickettsemia, the animal develops strong immunity against the agent, precluding a second rickettsemia.[20,21]

In Brazil, at least two animals are incriminated to act as efficient amplifier hosts for *A. cajennense*: capybaras and opossums (*Didelphis* spp.). Capybaras are abundant and act as primary hosts for *A. cajennense* in all RMSF-endemic areas of the state of São Paulo, where *A. cajennense* is the vector, in contrast to many other non-endemic areas for RMSF with abundant populations of *A. cajennense* sustained by horses in the absence of capybaras. Earlier studies in the 1940s showed that capybaras are susceptible to the *R. rickettsii* infection, with rickettsemia lasting for several weeks.[22] Capybaras are prolific, generating a mean of six pups per female per year.[23] Finally, a recent study in our laboratory has shown that after being experimentally infected with *R. rickettsii*, rickettsemic capybaras infected 20–25% of the *A. cajennense* nymphs that fed on them, as shown by PCR performed on the adult ticks that molted from the nymphs.[24]

Coupled to these evidences, the major environmental modification implicated to have contributed to the re-emergence of RMSF in the state of São Paulo is the explosive increase of capybara populations during the last few decades. There are no official numbers about the temporal distribution of capybaras

in São Paulo, however it is well known that this large rodent was considered threatened with extinction during the 1950s; during subsequent decades capybaras increased in populations in many areas, and nowadays it is considered a major cause of crop damage in the state,[25] besides various complaints of high environmental burdens by *A. cajennense* due to increased capybara populations. An increase in capybara populations is considered to be a result of extensive reforestation of areas near water courses (capybaras have a strong affinity to water, which they use for mating and avoiding predators) and strict laws prohibiting wildlife hunting in Brazil. Since these reforestation areas lack natural predators of capybaras (e.g., jaguars, anacondas, and alligators), and the nearby crops (e.g., corn, sugarcane) provide an abundant food supply, capybaras encountered an anthropogenic habitat where they can reach population densities much higher than those usually seen in its natural habitats in Pantanal and Amazon.[25]

Opossums (*Didelphis* spp.) are abundant in all RMSF-endemic areas of Brazil, where they can be infested by a large number of *A. cajennense* immature ticks, sometimes with close to 1,000 immature *Amblyomma* ticks (mostly *A. cajennense*) per opossum.[26] The susceptibility of opossums to the *R. rickettsii* infection has been demonstrated since the 1930s, when the first isolations of *R. rickettsii* from naturally infected wildlife were performed, being one from *Didelphis aurita* (reported as *Didelphis marsupialis*)[27] from the state of Minas Gerais and another from *D. aurita* from the state of São Paulo.[28] Interestingly, in the United States the opossum *Didelphis virginiana* was experimentally shown to develop a rickettsemia lasting for 3 to 4 weeks after being experimentally inoculated with *R. rickettsii*.[29] This has been the longest rickettsemic period ever reported for *R. rickettsii* infection; other animals develop rickettsemia usually lasting for 1 to 2 weeks.[18,20] Opossums are also prolific, the female births 5 to 9 young between 1 and 3 times per year. Finally, a recent study in our laboratory has shown that *R. rickettsii*-experimentally-infected opossums (*Didelphis aurita*) developed rickettsemia lasting for 3 to 4 weeks, when ~5–20% of the *A. cajennnense* immature ticks that fed on them became infected by *R. rickettsii*, as shown by PCR performed on the ticks after molting.[30]

For *A. aureolatum*, there is little available ecological information, although the rodent *Euryzygomatomys spinosus* is largely suspected to be an amplifier host for *R. rickettsii*. This rodent is abundant in RMSF-endemic areas in the São Paulo metropolitan area, where it is suspected to be a primary host for the immature stages of *A. aureolatum*.[31] *E. spinosus* is also a prolific species, but there is no available information regarding its susceptibility to *R. rickettsii*. However, *E. spinosus* is phylogenetically closely related to guinea pigs (*Cavea aperea porcellus*), as they both belong to the same Rodent infraorder, the Caviomorpha. Since guinea pigs are highly susceptible to *R. rickettsii* and also develop rickettsemia in a sufficient magnitude to infect feeding ticks,[18] it is possible that *E. spinosus* would give similar results and act as amplifier hosts for *R. rickettsii* in RMSF-endemic areas of the São Paulo metropolitan area, as suggested recently.[31]

In a recent study in our laboratory, each of six guinea pigs, experimentally infected with *R. rickettsii*, were simultaneously infested by larvae of *A. cajennense* and *A. aureolatum* (tick species were infested separately, into two feeding chambers glued to the back of each guinea pig). After feeding during the guinea pig febrile period, engorged larvae of the two species were collected and allowed to molt to nymphs in an incubator. The resultant nymphs were tested by PCR (10–20 nymphs per species per guinea pig) giving the following results: 80 to 100% of the *A. aureolatum* nymphs from six guinea pigs were PCR positive, whereas only 10 to 60% of the *A. cajennense* nymphs were PCR positive.[32] These results clearly indicate that *A. cajennense* are much less susceptible to the *R. rickettsii* infection, even after they fed on animals developing rickettsemia with sufficient magnitude to infect 100% of the *A. aureolatum* ticks. As an

important note, part of the *A. cajennense* ticks used in this study were derived from uninfected females collected in a RMSF-endemic area in the state of São Paulo, thus they represented a tick population that has been incriminated in transmitting *R. rickettsii* to humans. An ongoing study in our laboratory has also shown that *R. rickettsii* is moderately pathogenic for *A. aureolatum* ticks, especially engorged females (M. B. Labruna, unpublished data).

Considering that not all *A. cajennense* ticks become infected by *R. rickettsii* after feeding on a highly competent experimental amplifier host (i.e., guinea pig), the fact that only a minority of the *A. cajennense* ticks sustained the rickettsial infection after feeding on *R. rickettsii*-infected opossums or capybaras means that these wild animals are also competent amplifier hosts for *R. rickettsii*. This partial susceptibility of *A. cajennense* for *R. rickettsii* infection might explain why so few populations of this tick species are found naturally infected by *R. rickettsii*, despite its widespread distribution in central and southeastern Brazil. Also, it might explain the scarcity of human cases in RMSF-endemic areas where humans are often attacked by *A. cajennense*; usually in mass attack by hundreds or thousands of ticks. Interestingly, Parker and colleagues[14] showed under experimental conditions that *A. cajennense* was an efficient vector of *R. rickettsii,* with successful transstadial transmission of the agent. However, a subsequent study revealed that the *A. cajenennse* tick colony used in the study of Parker and colleagues[14] was, in fact, another tick species, described later as *Amblyomma imitator.*[33] Even though, Monteiro and Fonseca[34] demonstrated transovarial transmission, and Brumpt[35] demonstrated transstadial transmission of *R. rickettsii* in *A. cajennense*, but always without quantification analysis.

In contrast to *A. cajennense*, *A. aureolatum* seems to be a very efficient reservoir of *R. rickettsii* because usually 100% of the ticks became infected after feeding on a competent amplifier host (i.e., guinea pigs). In addition, Pinter and Labruna[36] reported 100% transstadial transmission (larvae to nymphs) of *R. rickettsii* in *A. aureolatum*. However, population densities of *A. aureolatum* are generally low, and humans are seldom infested by this tick. In a two-year study in a RMSF-endemic area of the São Paulo metropolitan area, dogs were found to be continuously infested by adults of *A. aureolatum*, with mean infestations around 2 ticks per dog; during this same period, human infestation was documented only once by a single tick specimen.[12] This might explain why RMSF cases are also sporadically reported even in this area, besides the high vectoral competence of *A. aureolatum*.

RMSF continues to be a threatening disease because high lethality rates are still occurring. The disease has shown to have a complex ecology with participation of different vertebrate animals and tick species from the United States to Argentina. Besides capybaras and opossums, other potential animal species have been implicated to act as amplifier hosts in Brazil, as is the case of rabbits (*Sylvilagus brasiliensis*) and the domestic dog.[37] More studies are needed to determine the role of the dog tick, *R. sanguineus,* in the ecology of RMSF in South America. This tick is widespread in all South American countries, and a recent study found *R. rickettsii*-infected *R. sanguineus* ticks in Brazil.[5] Further ecological studies in each of the RMSF-endemic areas are needed in order to understand the dynamics of the occurrence of the disease, and consequently, to generate subsidies for adoption of more rational preventive and control methods.

Rickettsia prowazekii and *Rickettsia typhi*

R. prowazekii is the etiologic agent of epidemic typhus, the second most severe rickettsiosis of the world. The only known vector of *R. prowazekii* in South America is the human body lice, *Pediculus humanus corporis.* During the last decades, the occurrence of epidemic typhus in South America has been confirmed only in Peru, especially in the Calca-Cuzco zones.[38] *R. prowazekii* is highly lethal for lice,

in which the bacterium is transstadially but not transovarially transmitted.[39] Unlike other rickettsiosis, humans surviving from *R. prowazekii*-acute infection usually develop asymptomatic latent infection for many years, with the possibility of a later recrudescence that could start new epidemics by infecting new lice. A recent study reported the isolation of *R. prowazekii* from *Amblyomma* ticks in Mexico, suggesting a participation of ticks in the ecology of epidemic typhus.[40]

The occurrence of *R. typhi* in South America has been reported since the first decades of the last century.[41] *R. typhi* is the etiologic agent of murine typhus, a rarely lethal, however, very incapacitating rickettsiosis. *R. typhi* is classically vectored by the flea species *Xenopsylla cheops,* but the occurrence of transovarial transmission of *R. typhi* in fleas seem to be a rare event.[42] *R. typhi* is widely distributed in the world, however, it has been largely neglected in South America during the last decades. Except for a few recent studies reporting endemic typhus in Brazil and Colombia,[43,44] there has been no clinical or ecological study of *R. typhi* in South America. This situation will possibly remain stable because there has been no interest of South American laboratories to implement proper techniques for diagnosis of TG rickettsia. For example, the Brazilian reference laboratories for the diagnosis of RMSF employ serological methods with SFG antigens, but most of the time no TG antigen is available. Since there is little or no cross-reactivity between TG and SFG rickettsiae, possibly several cases of TG rickettsiosis have been undiagnosed in Brazil.

Rickettsia parkeri

R. parkeri was first shown to cause spotted fever in humans in the United States in 2004, 65 years after this rickettsia was first isolated from the tick *Amblyomma maculatum* in that country.[45] Currently, *R. parkeri* is a recognized human pathogen with several confirmed cases in the United States, where it is transmitted by *A. maculatum*.[46,47] One retrospective study in the United States provided serological evidence, for a number of RMSF cases (presumably caused by *R. rickettsii*) were caused by *R. parkeri,* suggesting that rickettsiosis due to *R. parkeri* has been misidentified with RMSF in that country.[48] There has been convincing evidence that *R. parkeri* is the agent responsible for previously reported cases of SFG rickettsiosis in southern Uruguay, with transmission by the tick *Amblyomma triste*.[46,49]

Recent studies have shown that nearly 10% of both *A. maculatum* and *A. triste* ticks are infected by *R. parkeri* in the United States and Uruguay, respectively.[49,50] In the study of the United States, all tick populations tested were shown to be infected by *R. parkeri*, indicating that this agent is widely distributed among the *A. maculatum* distribution area in that country. One study in Brazil also reported ~10% infection rate by *R. parkeri* in an *A. triste* population, besides human infection by this agent in Brazil remains to be reported.[51] Overall, all populations of both *A. maculatum* and *A. triste* tested so far have been found infected by *R. parkeri.* Since *A. maculatum* is distributed from southern United States to the northwestern part of South America, whereas *A. triste* is likely to be established in most countries of South America,[52] it is possible that *R. parkeri* is also widely distributed in the Americas. Interestingly, these two tick species are morphologically, genetically, and ecologically very closely related, indicating that further studies are needed to test if they represent different strains of a single species or if they have just gone through speciation. Thus, human cases by *R. parkeri* in South America have been possibly undiagnosed or misdiagnosed with *R. rickettsii*, since this rickettsia seems to cause a milder disease culminating in no lethality to date, what turns even more difficult a definitive diagnosis.

The intimate relation of *R. parkeri* with its primary vectors, added by high infection rates among tick populations (if compared to *R. rickettsii*), are indicative that ticks are very efficient reservoirs of this rickettsia, although further

studies are needed to evaluate the role of amplifier hosts in the ecology of this rickettsia.

Rickettsia felis

Since the end of the last century, cases of flea-borne spotted fever have been reported throughout the world, implicating *R. felis* as the etiological agent.[53] Like its main host (fleas of the genus *Ctenocephalides*), *R. felis* seems to be cosmopolitan. In South America, *R. felis* has been reported infecting *Ctenocephalides* spp. fleas in Argentina, Brazil, Chile, Peru, and Uruguay, but human infection by *R. felis* has been reported only in Brazil so far.[54,55]

Laboratory studies showed that *R. felis* is successfully maintained in flea populations by transstadial and transovarial transmission.[56] Field studies with different *Ctenocephalides* spp. populations in the above-mentioned South American countries have shown that 13.5 to 90% of the individual fleas are infected by *R. felis*.[54,55] Indeed, such high infection rates indicate that *R. felis* is not pathogenic for fleas under natural conditions of South America.

Ctenocephalides fleas are the most prevalent and abundant fleas of dogs and cats in South America and possibly in the world. Since the vast majority of the *Ctenocephalides* populations are infected by *R. felis,* usually at high infection rates, one would expect that flea-borne spotted fever would occur more frequently than currently recognized. However, one study showed no serologic evidence of *R. felis* infection in dogs, cats, and opossums that were parasitized by *R. felis*-infected fleas in different areas of the state of São Paulo.[57] In another study, cats artificially infested by *R. felis*-infected fleas took a minimum of 2 to 4 months to seroconvert while other cats did not seroconvert, despite various previous contact with infected fleas.[58] A study in Chile showed serologic evidence of *R. felis* infection in 16/22 (72.7%) cats that sustained a *R. felis*-infected flea population.[54] These studies show that despite of the widespread distribution of *R. felis,* cases of human or animal infection by this agent are rare or irregular. Possibly, *Ctenocephalides* fleas are not a very efficient vector of *R. felis.* Previous analyses of infected fleas showed that *R. felis* colonizes the midgut, muscles, fat body, tracheal matrix, and reproduction organs, but not the salivary glands.[59] The presence of *R. felis* DNA in feces of infected fleas has also been reported.[56] A more recent study demonstrated the presence of *R. felis* in flea salivary glands for the first time, but it is not known if the agent is also present in flea saliva.[60] If *R. felis* is not transmitted via flea saliva, possible transmission mechanisms could be through the ingestion of infected fleas or contact of damaged skin or mucosa with fresh flea feces containing viable *R. felis*. In addition, it is possible that due to unknown reasons, only a minority of humans and animals are susceptible to the *R. felis* infection.

Other *Rickettsia* Species

Several other *Rickettsia* species have been reported infecting South American ticks recently (Table 1). All these rickettsia but *R. bellii* are considered to be SFG rickettsiae. No human infection by these rickettsiae has been reported in South America. The finding of *R. massiliae* in Argentina[61] deserves attention because until this report, *R. massiliae* was known to occur only in the Old World, where it was first described in 1993 infecting *Rhipicephalus* spp. ticks in Europe and Africa.[62] More than 10 years later, this rickettsia was first shown to be pathogenic for humans in Europe.[63] Due to the widespread distribution of *R. sanguineus* in South America, it is possible that undiagnosed or misdiagnosed cases of *R. massiliae* are occurring in this continent. Regarding the other rickettsiae described in Table 1, at least among animals, there has been serological evidence of canine infection by *Candidatus* "R. amblyommii" and *R. rhipicephali*,[64] and capybara infection by *R. bellii*.[8]

Since these other rickettsiae usually infect ticks at high infection rates (10 to 100%), they are possibly non-pathogenic for ticks. In

TABLE 1. Other *Rickettsia* spp. Reported Infecting Ticks in South America

Rickettsia	Tick species[Reference]	Country
R. rhipicephali	*Haemaphysalis juxtakochi*[67]	Brazil
R. bellii	*Amblyomma dubitatum* (reported as *A. cooperi*),[68] *A. aureolatum*,[4] *A. ovale*,[69] *A. oblongoguttatum*,[69] *A. rotundatum*,[69] *A. humerale*,[69] *A. scalpturatum*,[69] *A. neumanni*,[70] *H. juxtakochi*,[67] *Ixodes loricatus*[65]	Argentina, Brazil
R. massiliae	*Rhipicephalus sanguineus*[61]	Argentina
Candidatus "R. amblyommii"	*A. cajennense*,[69] *A. coelebs*,[69,71] *A. neumanni*[70]	Argentina, Brazil, French Guyana
Candidatus "R. andeanae"	*I. boliviensis*,[72] *A. maculatum*[72]	Peru
Rickettsia sp. strain Argentina	*A. parvum*[73]	Argentina
Rickettsia sp. strain COOPERI*	*A. dubitatum* (reported as *A. cooperi*)[68]	Brazil
Rickettsia sp. strain AL#	*A. longirostre*[74]	Brazil
Rickettsia sp. strain ARANHA#	*A. longirostre*[75]	Brazil

*This rickettsia is possibly a different strain of *R. parkeri*

#These rickettsiae are possibly different strains of *Candidatus* "R. amblyommii"

addition, transovarial transmission seems to be a rule for them, as it has been shown for *R. bellii* in *I. loricatus*.[65] These other rickettsiae might also have a role in the *R. rickettsii* ecology, since once prevailing at higher infection rates in some tick populations, these rickettsiae could prevent the establishment of *R. rickettsii* infection in these tick populations by the interference mechanism, as previously reported for some tick populations in the United States.[13,66]

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Conflicts of Interest

The author declares no conflicts of interest.

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